



#15

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/319,156
Source: 1648
Date Processed by STIC: 2/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

09/319,156

ad

Application No.: _____

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An ~~initial~~ or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

For CRF Submission Help, call (703) 308-4212

For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

#13

1648

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/319,156

TIME: 12:42:40

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

see
P.5Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: PARANHOS-BACCALA, Glaucia
 4 KOMURIAN-PRADEL, Florence
 5 BEDIN, Frederic
 6 SODOYER, Mireille
 7 OTT, Catherine
 8 MALLET, Francois
 9 PERRON, Herve
 10 MANDRAND, Bernard
 12 <120> TITLE OF INVENTION: RETROVIRAL NUCLEIC MATERIAL AND NUCLEOTIDE FRAGMENTS, IN
 PARTICULAR,
 13 ASSOCIATED WITH MULTIPLE SCLEROSIS AND/OR RHEUMATOID ARTHRITIS, FOR DIAGNOSTIC,
 14 PROPHYLACTIC AND THERAPEUTIC USES
 16 <130> FILE REFERENCE: 103514
 18 <140> CURRENT APPLICATION NUMBER: US/09/319,156
 19 <141> CURRENT FILING DATE: 1999-11-02
 21 <150> PRIOR APPLICATION NUMBER: PCT/FR98/01460
 22 <151> PRIOR FILING DATE: 1998-07-07
 24 <150> PRIOR APPLICATION NUMBER: FR/97/08816
 25 <151> PRIOR FILING DATE: 1997-07-07
 27 <160> NUMBER OF SEQ ID NOS: 45
 29 <170> SOFTWARE: PatentIn version 3.0
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 32 <211> LENGTH: 34
 33 <212> TYPE: DNA
 34 <213> ORGANISM: MSRV
 36 <400> SEQUENCE: 1
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 43 <213> ORGANISM: MSRV
 45 <400> SEQUENCE: 2
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 52 <213> ORGANISM: MSRV
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 59 <211> LENGTH: 310
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 61 <213> ORGANISM: MSRV
 63 <400> SEQUENCE: 4
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 68 agccactgag gaaggaaaaa tactttcacc tgcagctaac caacagaaat tacttaaaac 180
 70 ccttcaccaa accttcocact taggcattga tagcacccat cagatggcca aattattatt 240

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/319,156

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TIME: 12:42:40

Input Set : A:\es.txt
Output Set: N:\CRF3\07252001\I319156.raw

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83 <221> NAME/KEY: misc_feature
84 <222> LOCATION: (26)..(26)
85 <223> OTHER INFORMATION: Xaa = any amino acid
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91 1 5 10 15
93 Pro Gln Tyr Ser Ala Gly Lys Ile Glu Xaa Glu Thr Ser Gln Gly His
94 20 25 30
96 Thr Phe Leu Pro Ser Arg Trp Leu Ala Thr Glu Glu Gly Lys Ile Leu
97 35 40 45
99 Ser Pro Ala Ala Asn Gln Gln Lys Leu Leu Lys Thr Leu His Gln Thr
100 50 55 60
102 Phe His Leu Gly Ile Asp Ser Thr His Gln Met Ala Lys Leu Leu Phe
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121 ctggaccggc ctgctagccc atgctccgat gttaatgaca ttgaaggcac ccctcccag      180
123 gaaatctcaa ctgcacaacc cctactatgc cccaattcag cggaagcag ttagagcggt      240
125 catcagccaa cctccccaac agcacttggg ttttctgtt gagagggggg actgagagac      300
127 aggactagct ggatttcta ggccaacgaa gaatccctaa gcctagctgg gaaggtgact      360
129 gcatccacct ctaaactatg ggcttgcaac ttagctcaca cccgaccaat cagagagctc      420
131 actaaaatgc taattaggca aaaataggag gtaaagaaat agccaatcat ctattgcctg      480
133 agagcacagc gggagggaca aggatcgga tataaaccca ggcattcgag ccggcaacgg      540
135 caacccctt tgggtccctt ccctttgtat gggcgctctg ttttcactct atttcactct      600
137 attaaatctt gcaactgaaa aaaaaaaaaa aaaaa      635
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 77
142 <212> TYPE: PRT
143 <213> ORGANISM: MSRV
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148 1 5 10 15
150 Thr Val Lys Leu Gln Ile Val Leu Gln Met Glu His Gln Met Glu Ser

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/319,156

DATE: 07/25/2001
TIME: 12:42:40

Input Set : A:\es.txt
Output Set: N:\CRF3\07252001\I319156.raw

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153 Met Thr Lys Ile His Arg Gly Pro Leu Asp Arg Pro Ala Ser Pro Cys
154          35          40          45
156 Ser Asp Val Asn Asp Ile Glu Gly Thr Pro Pro Glu Glu Ile Ser Thr
157          50          55          60
159 Ala Gln Pro Leu Leu Cys Pro Asn Ser Ala Gly Ser Ser
160 65          70          75
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163 <211> LENGTH: 32
164 <212> TYPE: DNA
165 <213> ORGANISM: MSRV
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172 <211> LENGTH: 1481
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181 acgcggtctt ctggaaatat tgatgcccc aactgctata actctgccac tctttgcatg      180
183 accttcaactg cccacaccca tatgccccgc aactgctata actctgccac tctttgcatg      240
185 catgcaaata ctcatatttg gacagggaaa atgattaatc ctagtgtgcc tggaggactt      300
187 ggagccactg tctgttggac ttacttcacc cataccagta tgtctgatgg ggttggaatt      360
189 caaggtcagg caagagaaaa acaagtaaag gaagcaatct cccaactgac ccggggacat      420
191 agcaccctta gccctacaaa aggactagtt ctctcaaaac tacatgaaac cctccgtacc      480
193 catactgcc tgggtgagct atttaatacc accctcactc ggtccatga ggtctcagcc      540
195 caaaacctta ctaactgttg gatgtgcctc cccctgcact tcaggccata catttcaatc      600
197 cctgttcttg aacaatggaa caacttcagc acagaaataa acaccacttc cgttttagta      660
199 ggacctcttg tttccaatct ggaaataacc catacctcaa acctcacctg tgtaaaattt      720
201 agcaatacag tagacacaac cagctcccaa tgcacaggt gggtaacacc tcccacacga      780
203 atagtctgcc taccctcagg aatatttttt gtctgtggta cctcagccta tcattgtttg      840
205 aatggctctt cagaatctat gtgcttcctc tcattcttag tgccccctat gaccatctac      900
207 actgaacaag atttatacaa tcatgtcgta cctaagcccc acaacaaaag agtaccatt      960
209 ctctcttttg ttatcagagc aggagtgcga ggcagactag gtactggcat tggcagtatc      1020
211 acaacctcta ctcaattcta ctacaaacta tctcaagaaa taaatgggtga catggaacag      1080
213 gtcactgact ccctgggtcac cttgcaagat caacttaact ccctagcagc agtagtcctt      1140
215 caaaatcgaa gagcttttaga cttgctaacc gccaaaagag ggggaacctg tttattttta      1200
217 ggagaagaac gctgttatta tgttaataca tccagaattg tcaactgagaa agttaaaagaa      1260
219 attcgagatc gaatacaatg tagagcagag gagcttcaaa acaccgaacg ctggggcctc      1320
221 ctcaagccaa ggatgccctg ggttctcccc ttcttaggac ctctagcagc tctaataattg      1380
223 ttactcctct ttggaccctg tatctttaac ctcttggtta agtttgtctc ttccagaatt      1440
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229 <211> LENGTH: 493
230 <212> TYPE: PRT
231 <213> ORGANISM: MSRV
233 <220> FEATURE:
234 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING
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235 <222> LOCATION: (39)..(39)
 236 <223> OTHER INFORMATION: Xaa = any amino acid
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 242 1 5 10 15
 244 Phe Ala Leu Thr Ala Pro Pro Pro Cys Cys Cys Thr Thr Ser Ser Ser
 245 20 25 30
 247 Pro Tyr Gln Glu Phe Leu Xaa Arg Thr Arg Leu Pro Gly Asn Ile Asp
 248 35 40 45
 250 Ala Pro Ser Tyr Arg Ser Leu Ser Lys Gly Asn Ser Thr Phe Thr Ala
 251 50 55 60
 253 His Thr His Met Pro Arg Asn Cys Tyr Asn Ser Ala Thr Leu Cys Met
 254 65 70 75 80
 256 His Ala Asn Thr His Tyr Trp Thr Gly Lys Met Ile Asn Pro Ser Cys
 257 85 90 95
 259 Pro Gly Gly Leu Gly Ala Thr Val Cys Trp Thr Tyr Phe Thr His Thr
 260 100 105 110
 262 Ser Met Ser Asp Gly Gly Gly Ile Gln Gly Gln Ala Arg Glu Lys Gln
 263 115 120 125
 265 Val Lys Glu Ala Ile Ser Gln Leu Thr Arg Gly His Ser Thr Pro Ser
 266 130 135 140
 268 Pro Tyr Lys Gly Leu Val Leu Ser Lys Leu His Glu Thr Leu Arg Thr
 269 145 150 155 160
 271 His Thr Arg Leu Val Ser Leu Phe Asn Thr Thr Leu Thr Arg Leu His
 272 165 170 175
 274 Glu Val Ser Ala Gln Asn Pro Thr Asn Cys Trp Met Cys Leu Pro Leu
 275 180 185 190
 277 His Phe Arg Pro Tyr Ile Ser Ile Pro Val Pro Glu Gln Trp Asn Asn
 278 195 200 205
 280 Phe Ser Thr Glu Ile Asn Thr Thr Ser Val Leu Val Gly Pro Leu Val
 281 210 215 220
 283 Ser Asn Leu Glu Ile Thr His Thr Ser Asn Leu Thr Cys Val Lys Phe
 284 225 230 235 240
 286 Ser Asn Thr Ile Asp Thr Thr Ser Ser Gln Cys Ile Arg Trp Val Thr
 287 245 250 255
 289 Pro Pro Thr Arg Ile Val Cys Leu Pro Ser Gly Ile Phe Phe Val Cys
 290 260 265 270
 292 Gly Thr Ser Ala Tyr His Cys Leu Asn Gly Ser Ser Glu Ser Met Cys
 293 275 280 285
 295 Phe Leu Ser Phe Leu Val Pro Pro Met Thr Ile Tyr Thr Glu Gln Asp
 296 290 295 300
 298 Leu Tyr Asn His Val Val Pro Lys Pro His Asn Lys Arg Val Pro Ile
 299 305 310 315 320
 301 Leu Pro Phe Val Ile Arg Ala Gly Val Leu Gly Arg Leu Gly Thr Gly
 302 325 330 335
 304 Ile Gly Ser Ile Thr Thr Ser Thr Gln Phe Tyr Tyr Lys Leu Ser Gln
 305 340 345 350
 307 Glu Ile Asn Gly Asp Met Glu Gln Val Thr Asp Ser Leu Val Thr Leu
 308 355 360 365

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310 Gln Asp Gln Leu Asn Ser Leu Ala Ala Val Val Leu Gln Asn Arg Arg
311      370                      375                      380
313 Ala Leu Asp Leu Leu Thr Ala Lys Arg Gly Gly Thr Cys Leu Phe Leu
314 385                      390                      395                      400
316 Gly Glu Glu Arg Cys Tyr Tyr Val Asn Gln Ser Arg Ile Val Thr Glu
317                      405                      410                      415
319 Lys Val Lys Glu Ile Arg Asp Arg Ile Gln Cys Arg Ala Glu Glu Leu
320                      420                      425                      430
322 Gln Asn Thr Glu Arg Trp Gly Leu Leu Ser Gln Trp Met Pro Trp Val
323                      435                      440                      445
325 Leu Pro Phe Leu Gly Pro Leu Ala Ala Leu Ile Leu Leu Leu Phe
326      450                      455                      460
328 Gly Pro Cys Ile Phe Asn Leu Leu Val Lys Phe Val Ser Ser Arg Ile
329 465                      470                      475                      480
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332                      485                      490

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334 <210> SEQ ID NO: 11

335 <211> LENGTH: 32

336 <212> TYPE: DNA

337 <213> ORGANISM: MSRV

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32

343 <210> SEQ ID NO: 12

344 <211> LENGTH: 1329

345 <212> TYPE: DNA

346 <213> ORGANISM: MSRV

348 <220> FEATURE:

349 <221> NAME/KEY: misc_feature

350 <222> LOCATION: (1232)..(1232)

351 <223> OTHER INFORMATION: n = a, g, c or t/u

354 <400> SEQUENCE: 12

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355 tcaaaatcga agagcttttag acttgctaac cgccaaaaga gggggaacct gtttattttt      60
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359 aatttgagat cgaatataat gtagagcaga ggaccttcaa aacactgcac cctggggcct      180
361 cctcagccaa tggatgccct ggactctccc cttcttagga cctctagcag ctataatatt      240
363 tttactcttc tttggacctt gtatcttcaa cttccttggt aagtgtgtct cttccagaat      300
365 tgaagctgta aagctacaaa tagttcttca aatggaacct cagatgcagt ccatgactaa      360
367 aatctaccgt ggacctctgg accggcctgc tagactatgc tctgatgta atgacattga      420
369 agtcaccctt cccgaggaaa tctcaactgc acaaccctta ctacactcca attcagtagg      480
371 aagcagtttag agcagttgtc agccaacctc cccaacagta cttgggtttt cctgttgaga      540
W--> 373 ggggtggactg agagacagga cttagctggat ttcttaggct gactaagaat cccaagcct      600
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377 accaatcaga gagctcacta aaatgctaata caggcaaaaa caggaggtaa agcaatagcc      720
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381 ttcaagccag caacagcaac cccctttggg tcccctccca ttgtatggga gctctgtttt      840
383 cactctattt cactctatta aatcatgcaa ctgcactctt ctggctccgtg ttttttatgg      900
385 ctcaagctga gcttttgttc gccatccacc actgctgttt gccaccgtca cagaccgct      960
387 gctgacttcc atccctttgg atccagcaga gtgtccactg tgctcctgat ccagcgaggt      1020
389 aoccattgcc actcccgatc aggctaaagg cttgccattg ttctgcatg gctaagtgcc      1080

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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/319,156

DATE: 07/25/2001

TIME: 12:42:41

Input Set : A:\es.txt

Output Set: N:\CRF3\07252001\I319156.raw

L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:247 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:373 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40